SEQUENCE LISTING

<110> MACK, DAVID
GISH, KURT

<120> NOVEL METHODS OF DIAGNOSING AND TREATING BREAST CANCER, COMPOSITIONS, AND METHODS OF SCREENING FOR BREAST CANCER MODULATORS

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gcgagcgctg ccgctggatc ctgcccctgc tcctactcag cgccatcgcc ttcgacatca 180
tcgcgctggc cggccgcggc tggttgcagt ctagcgacca cggccagacg tcctcgctgt 240
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tcatggagta cgcgtggggt agagcagcgg ctgccatgct cttctgtggc ttcatcatcc 360
tggtgatctg tttcatcctc tccttcttcg ccctctgtgg accccagatg cttgtcttcc 420
tgagagtgat tggaggtctc cttgccttgg ctgctgtgtt ccagatcatc tccctggtaa 480
tttaccccgt gaagtacacc cagaccttca cccttcatgc caaccctgct gtcacttaca 540
tctataactg ggcctacggc tttgggtggg cagccacgat tatcctgatt ggctgtgcct 600
tcttcttctg ctgcctcccc aactacgaag atgaccttct gggcaatgcc aagcccaggt 660
acttctacac atctgcctaa cttgggaatg aatgtgggag aaaatcgctg ctgctgagat 720
ggactccaga agaagaaact gtttctccag gcgactttga acccattttt tggcagtgtt 780
catattatta aactagtcaa aaatgctaaa ataatttggg agaaaatatt ttttaagtag 840
tgttatagtt tcatgtttat cttttattat gttttgtgaa gttgtgtctt ttcactaatt 900
acctatacta tgccaatatt tccttatatc tatccataac atttatacta catttgtaag 960
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atatcatttg tgagaatttc tcattaatat cctgaatcat tcattttagc taaggcttca 1260
tgttgactcg atatgtcatc taggaaagta ctatttcatg gtccaaacct gttgccatag 1320
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atgttcagaa ccagagtaga ctggattgaa agatggactg ggtctaattt atcatgactg 1500
atagatctgg ttaagttgtg tagtaaagca ttaggagggt cattcttgtc acaaaagtgc 1560
cactaaaaca gcctcaggag aataaatgac ttgcttttct aaatctcagg tttatctggg 1620
ctctatcata tagacaggct tctgatagtt tgcaactgta agcagaaacc tacatatagt 1680
taaaatcctg gtctttcttg gtaaacagat tttaaatgtc tgatataaaa catgccacag 1740
gagaattcgg ggatttgagt ttctctgaat agcatatata tgatgcatcg gataggtcat 1800
tatgattttt taccatttcg acttacataa tgaaaaccaa ttcattttaa atatcagatt 1860
attattttgt aagttgtgga aaaagctaat tgtagttttc attatgaagt tttcccaata 1920
aaccaggtat tctaaacttg aaaaaaaaaa aaaaaaaa 1958

<210> 12
<211> 582
<212> DNA
<213> Homo sapiens

<400> 12
atgatccgct gcggcctggc ctgcgagcgc tgccgctgga tcctgcccct gctcctactc 60
agcgccatcg ccttcgacat catcgcgctg gccggccgcg gctggttgca gtctagcgac 120
cacggccaga cgtcctcgct gtggtggaaa tgctcccaag agggcggcgg cagcgggtcc 180

tacgaggagg gctgtcagag cctcatggag tacgcgtggg gtagagcagc ggctgccatg 240
ctcttctgtg gcttcatcat cctggtgatc tgtttcatcc tctccttctt cgccctctgt 300
ggaccccaga tgcttgtctt cctgagagtg attggaggtc tccttgcctt ggctgctgtg 360
ttccagatca tctccctggt aatttacccc gtgaagtaca cccagacctt caccttcat 420
gccaaccctg ctgtcactta catctataac tgggcctacg gctttgggtg ggcagccacg 480
attatcctga ttggctgtgc cttcttcttc tgctgcctcc ccaactacga agatgacctt 540
ctgggcaatg ccaagcccag gtacttctac acatctgcct aa 582

<210> 13
<211> 193
<212> PRT
<213> Homo sapiens

<400> 13
Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro
1 5 10 15

Leu Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly
20 25 30

Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln Thr Ser Ser Leu Trp
35 40 45

Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly Ser Tyr Glu Glu Gly
50 55 60

Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg Ala Ala Ala Ala Met
65 70 75 80

Leu Phe Cys Gly Phe Ile Ile Leu Val Ile Cys Phe Ile Leu Ser Phe
85 90 95

Phe Ala Leu Cys Gly Pro Gln Met Leu Val Phe Leu Arg Val Ile Gly
100 105 110

Gly Leu Leu Ala Leu Ala Ala Val Phe Gln Ile Leu Ser Leu Val Ile
115 120 125

Tyr Pro Val Lys Tyr Thr Gln Thr Phe Thr Leu His Ala Asn Pro Ala
130 135 140

Val Thr Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr
145 150 155 160

Ile Ile Leu Ile Gly Cys Ala Phe Phe Phe Cys Cys Leu Pro Asn Tyr
165 170 175

Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro Arg Tyr Phe Tyr Thr Ser
180 185 190

Ala

<210> 14
<211> 193
<212> PRT
<213> Mouse

<400> 14
Met Leu Arg Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro
1 5 10 15

Leu Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly
20 25 30

Arg Gly Trp Leu Gln Ser Ser Asn His Ile Gln Thr Ser Ser Leu Trp
35 40 45

Trp Arg Cys Phe Asp Glu Gly Gly Gly Ser Gly Ser Tyr Asp Asp Gly
50 55 60

Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg Ala Ala Ala Ala Thr
65 70 75 80

Leu Phe Cys Gly Phe Ile Ile Leu Cys Ile Cys Phe Ile Leu Ser Phe
85 90 95

Phe Ala Leu Cys Gly Pro Met Gln Leu Val Phe Leu Arg Val Ile Gly
100 105 110

Gly Leu Leu Ala Leu Ala Ala Ile Phe Gln Ile Leu Ser Leu Val Ile
115 120 125

Tyr Pro Val Lys Tyr Thr Gln Thr Phe Arg Leu His Asp Asn Pro Ala
130 135 140

Val Asn Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr
145 150 155 160

Ile Ile Leu Ile Gly Cys Ser Phe Phe Phe Cys Cys Leu Pro Asn Tyr
165 170 175

Glu Asp Asp Leu Leu Gly Ala Ala Lys Pro Arg Tyr Phe Tyr Pro Pro
180 185 190

Ala

<210> 15
<211> 124
<212> PRT
<213> Rat

<400> 15
Glu Tyr Ala Trp Gly Arg Ala Ala Ala Ala Thr Leu Phe Cys Gly Phe
1 5 10 15

Ile Ile Leu Val Ile Cys Phe Ile Leu Ser Phe Phe Ala Leu Cys Gly
20 25 30

Pro Gln Met Leu Val Phe Leu Arg Val Ile Gly Gly Leu Leu Ala Leu
35 40 45

Ala Ala Val Phe Gln Ile Ile Ser Leu Val Ile Tyr Pro Val Lys Tyr
50 55 60

Thr Gln Thr Phe Arg Leu His Asp Asn Pro Ala Val Asn Tyr Ile Tyr
65 70 75 80

Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr Ile Ile Leu Ile Gly
85 90 95

Cys Ser Phe Phe Phe Cys Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu
100 105 110

Gly Asn Ala Lys Pro Arg Tyr Phe Tyr Thr Ser Ala
115 120

<210> 16
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 16
Cys Ser Tyr Ser Ala Pro Ser Pro Ser Thr Ser Ser Arg Trp Pro
1 5 10 15

<210> 17
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 17
Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro
1 5 10 15

<210> 18
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 18
Cys Gly Gly Asn Ala Pro Lys Arg Gly Gly Gly Arg Gly Ser Tyr
1 5 10 15

<210> 19
<211> 1970
<212> DNA
<213> Mouse

<400> 19
gtcaccggaa tcaaggtgtg gctggagcgc cgctcccccg ccgycagccc gkkggccgcg 60
tcttcggggg agccgcctct tccttwattc ggckcygaca gcgctcgcag gaccactctt 120
ggccgctgct cctgcccggc gttcctccgc tccgcgcccg ccgccaccga cgacatgctg 180
cgctgcggcc tggcctgcga gcgctgcagg tggatcctgc ccctgctgct gctcagcgcc 240
atcgccttcg acatcatcgc gctggccggc cgcggctggc tgcagtctag caaccacatc 300
cagacatcgt cgctttggtg gaggtgtttc gacgagggcg gcggcagcgg ctcctacgac 360
gatggctgcc agagcctcat ggagtacgca tggggacgag cagctgcagc cacgcttttc 420
tgtggcttta tcatcctgtg catctgcttc attctctcgt tcttcgccct gtgtggaccc 480
cagatgcttg ttttcctgag agtcattgga ggcctcctcg cactggctgc catattccag 540
atcatctccc tggtaatcta ccccgtgaag tacacacaga ccttcaggct tcacgataac 600
cctgctgtta attacatcta taactgggcc tatggcttcg gatgggcggc caccatcatc 660
ttgattggtt gttccttctt cttctgctgc ctccccaact acgaggatga ccttttgggg 720
gccgccaagc ccaggtactt ctatccccca gcctaatgtg ggaggaagag cctgagaaaa 780
gcctgctgca agatggatct gaggaggaaa ctgttctcca aggcacaagg aacctacgtt 840
tgggcaatgt tcatatgatc agaaatgtta gaataaatgc taaagaaaat tcttcataat 900

tagtgttaag tttcatgtat gtcgtgtgga gttaaaaaga cttgaattct gtttgctaag 960
tatatgctaa tttttcctta tgtcaattct ataccattta agcttcattt gttaaagaat 1020
atgcctgtga aacttgataa ggtagaaatg gagcagcctc tcatttaata atctgatggg 1080
gcttctgttt ttccacatag aatgggttgt ttctgctaag ggctacagag gaggaaagtc 1140
actggcaaaa cttccatgac caaatatcct gaaattagtt tgtttttttt taaaagacct 1200
tattttgagt tttcagttac ataaagaagc agaagcagat tggtttccta agtgagcatc 1260
atttgtgaga atttttagtc agtgttttga acaattattg tttttctaag cttcatgttg 1320
actttctctg atgcgtagaa aagtgttcta acgtggctga ggttaagccg ctgtcattac 1380
tgaaatgcta agaattttcc tcttttcccg tagtgtagag gggtagggtg tgggcagaag 1440
ccgtgttagc acatctgtag tattgtgtgt gtatgcttag aaccagcgta gaccggatgg 1500
gaggatggac taggcctaat ccctcccaac tggtggatgt gaagaggtca ggtaggaagg 1560
cacaggaggg tcaccactgt cacagcagtg ccatgcagac atcctaggag aagacatggc 1620
agtgtttctt ctcagtgctt cttcccttaa ctgagctctg ctcacagaca gctagaatag 1680
attttaactg aaacagaaac ctaaatgtaa ttaaaaacct ggtcttcctt ggtaagcaga 1740
cttaaaatat ctgtatagta catgcaagtg gaaaatttgg gaatgcgtgt ctctgaatac 1800
ataccggaag ggctactatt acctttttct taccatttat acttacctaa tggaaacgag 1860
cttgttttaa ctatcagaac actattttgt aaggtgctgc aaagacagtt gaagttttca 1920
ttaccaattt ccccaataaa ccaggtgttc aaatcctgaa aaaaaaaggc 1970

<210> 20
<211> 582
<212> DNA
<213> Mouse

<400> 20
atgctgcgct gcggcctggc ctgcgagcgc tgcaggtgga tcctgcccct gctgctgctc 60
agcgccatcg ccttcgacat catcgcgctg gccggccgcg gctggctgca gtctagcaac 120
cacatccaga catcgtcgct ttggtggagg tgtttcgacg agggcggcgg cagcggctcc 180
tacgacgatg gctgccagag cctcatggag tacgcatggg gacgagcagc tgcagccacg 240
cttttctgtg gctttatcat cctgtgcatc tgcttcattc tctcgttctt cgccctgtgt 300
ggaccccaga tgcttgtttt cctgagagtc attggaggcc tcctcgcact ggctgccata 360
ttccagatca tctccctggt aatctacccc gtgaagtaca cacagacctt caggcttcac 420
gataaccctg ctgttaatta catctataac tgggcctatg gcttcggatg ggcggccacc 480
atcatcttga ttggttgttc cttcttcttc tgctgcctcc ccaactacga ggatgacctt 540
ttgggggccg ccaagcccag gtacttctat cccccagcct aa 582

<210> 21
<211> 536
<212> DNA
<213> Rat

<400> 21
gaatacgcct ggggccgagc agctgctgcc actctcttct gtggattcat catcctggtc 60
atctgcttca tcctctcgtt cttcgccctg tgtggacccc agatgcttgt tttcctgaga 120
gtgattggag gccttctcgc actggctgct gtattccaga tcatctccct ggttatctat 180
cccgtgaagt acacacaaac cttcaggctt catgataatc ccgctgttaa ttacatctac 240

aactgggcct atggcttcgg atgggcagcc acgatcatct tgattggttg ctctttcttc 300
ttctgctgcc tccccaacta cgaggatgac cttctgggca atgcaaagcc caggtacttc 360
tatacatctg cctaatgtgg agggagatcc tgagaaaagc ctgctgcaag atgcatgtga 420
ggaggaaagt gttctccaag gagcaaagaa cctatgtttg ggcagtgttc atatgagtgg 480
aaatgctaga ataaatgcta aagaaaattc ttcataaaaa aaaaaaaaaa aaaaaa 536

<210> 22
<211> 375
<212> DNA
<213> Rat

<400> 22
gaatacgcct ggggccgagc agctgctgcc actctcttct gtggattcat catcctggtc 60
atctgcttca tcctctcgtt cttcgccctg tgtggacccc agatgcttgt tttcctgaga 120
gtgattggag gccttctcgc actggctgct gtattccaga tcatctccct ggttatctat 180
cccgtgaagt acacacaaac cttcaggctt catgataatc ccgctgttaa ttacatctac 240
aactgggcct atggcttcgg atgggcagcc acgatcatct tgattggttg ctctttcttc 300
ttctgctgcc tccccaacta cgaggatgac cttctgggca atgcaaagcc caggtacttc 360
tatacatctg cctaa 375

<210> 23
<211> 471
<212> DNA
<213> Homo sapiens

<400> 23
ctttgaagca tttttgtctg tgctccctga tcttcaggtc accaccatga agttcttagc 60
agtcctggta ctcttgggag tttccatctt tctggtctct gcccagaatc cgacaacagc 120
tgctccagct gacacgtatc cagctactgg tcctgctgat gatgaagccc ctgatgctga 180
aaccactgct gctgcaacaa ctgcgaccac tgctgctcct accactgcaa ccaccgctgc 240
ttctaccact gctcgtaaag acattccagt tttacccaaa tgggttgggg atctcccgaa 300
tggtagagtg tgtccctgag atggaatcag cttgagtctt ctgcaattgg gtcacaacta 360
ttcatgcttc ctgtgatttc atccaactac ttaccttgcc tacgatatcc cctttatctc 420
taatcagttt attttctttc aaataaaaaa taactatgag cgagctaaca t 471

<210> 24
<211> 273
<212> DNA
<213> Homo sapiens

<400> 24
atgaagttct tagcagtcct ggtactcttg ggagtttcca tctttctggt ctctgcccag 60
aatccgacaa cagctgctcc agctgacacg tatccagcta ctggtcctgc tgatgatgaa 120
gcccctgatg ctgaaaccac tgctgctgca accactgcga ccactgctgc tcctaccact 180
gcaaccaccg ctgcttctac cactgctcgt aaagacattc cagttttacc caaatgggtt 240

ggggatctcc cgaatggtag agtgtgtccc tga 273

<210> 25
<211> 90
<212> PRT
<213> Homo sapiens

<400> 25
Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile Phe Leu
1 5 10 15

Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr Tyr Pro
20 25 30

Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu Thr Thr Ala
35 40 45

Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr Ala Thr Thr Ala
50 55 60

Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val Leu Pro Lys Trp Val
65 70 75 80

Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
85 90

<210> 26
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 26
Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr Tyr Pro Ala Cys
1 5 10 15

<210> 27
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 27
Leu Pro Lys Trp Val Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
1 5 10 15

<210> 28
<211> 1555
<212> DNA
<213> Homo sapiens

<400> 28
ggagttttct ggagctgttg caatgtgtat gctggtgaaa tctacttgag cattaagcag 60
tatctcccag cattgttagc tactgagtgg cacatcttca gtacgcatga ttcgtggggg 120
actcaggcag aggtaaaagt gtgaaacttt tcagcattac ctaagaagca aaggctcaat 180
tttggctgct tcattcttat ctcttctgcc acagttctaa cgtgcctgat ctactgagac 240
caaggatgac caatgactca gaagggaaaa tgggatttaa acacccaaag atcatgggga 300
atttcagagg tcatgccctc cctggaacct tctttttttat tattggtctt tggtggtgta 360
caaagagtat tctgaagtat atctgcaaaa agcaaaagcg aacctgctat cttggttcca 420
aaacattatt ctatcgattg gaaattttgg agggaattac aatagttggc atggctttaa 480
ctggcatggc tggggagcag tttattcctg gagggcccca tctgatgtta tatgactata 540
aacaaggtca ctggaatcaa ctcctgggct ggcatcattt caccatgtat ttcttctttg 600
ggctgttggg tgtggcagat atcttatgtt tcaccatcag ttcacttcct gtgtccttaa 660
ccaagttaat gttgtcaaat gccttatttg tggaggcctt tatcttctac aaccacactc 720
atggccggga aatgctggac atctttgtgc accagctgct ggttttggtc gtctttctga 780
caggcctcgt tgccttccta gagttccttg ttcggaacaa tgtacttctg gagctattgc 840
ggtcaagtct cattctgctt caggggagct ggttctttca gattggattt gtcctgtatc 900
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tatgcttttg ttggcattat gcagtaacca ttgtcatcgt tggaatgaat tatgctttca 1020
ttacctggtt ggttaaatct agacttaaga ggctctgctc ctcagaagtt ggacttctga 1080
aaaatgctga acgagaacaa gaatcagaag aagaaatgtg actttgatga gcttccagtt 1140
tttctagata aacctttttct ttttttacatt gttcttggtt ttgtttctcg atcttttgtt 1200
tggagaacag ctggctaagg atgactctaa gtgtactgtt tgcatttcca atttggttaa 1260
agtatttgaa tttaaatatt ttctttttag ctttgaaaat attttgggtg atactttcat 1320
tttgcacatc atgcacatca tggtattcag gggctagagt gatttttttc cagattatct 1380
aaagttggat gcccacacta tgaaagaaat atttgtttta tttgccttat agatatgctc 1440
aaggttactg ggcttgctac tatttgtaac tccttgacca tggaattata cttgtttatc 1500
ttgttgctgc aatgagaaat aaatgaatgt atgtattttg gtgcagaaaa aaaaa 1555

<210> 29
<211> 291
<212> PRT
<213> Homo sapiens

<400> 29
Met Thr Asn Asp Ser Glu Gly Lys Met Gly Phe Lys His Pro Lys Ile
1 5 10 15

Met Gly Asn Phe Arg Gly His Ala Leu Pro Gly Thr Phe Phe Phe Ile
20 25 30

Ile Gly Leu Trp Trp Cys Thr Lys Ser Ile Leu Lys Tyr Ile Cys Lys
35 40 45

Lys Gln Lys Arg Thr Cys Tyr Leu Gly Ser Lys Thr Leu Phe Tyr Arg
50 55 60

Leu Glu Ile Leu Glu Gly Ile Thr Ile Val Gly Met Ala Leu Thr Gly
65 70 75 80

Met Ala Gly Glu Gln Phe Ile Pro Gly Gly Pro His Leu Met Leu Tyr
85 90 95

Asp Tyr Lys Gln Gly His Trp Asn Gln Leu Leu Gly Trp His His Phe
100 105 110

Thr Met Tyr Phe Phe Phe Gly Leu Leu Gly Val Ala Asp Ile Leu Cys
115 120 125

Phe Thr Ile Ser Ser Leu Pro Val Ser Leu Thr Lys Leu Met Leu Ser
130 135 140

Asn Ala Leu Phe Val Glu Ala Phe Ile Phe Tyr Asn His Thr His Gly
145 150 155 160

Arg Glu Met Leu Asp Ile Phe Val His Gln Leu Leu Val Leu Val Val
165 170 175

Phe Leu Thr Gly Leu Val Ala Phe Leu Glu Phe Leu Val Arg Asn Asn
180 185 190

Val Leu Leu Glu Leu Leu Arg Ser Ser Leu Ile Leu Leu Gln Gly Ser
195 200 205

Trp Phe Phe Gln Ile Gly Phe Val Leu Tyr Pro Pro Ser Gly Gly Pro
210 215 220

Ala Trp Asp Leu Met Asp His Glu Asn Ile Leu Phe Leu Thr Ile Cys
225 230 235 240

Phe Cys Trp His Tyr Ala Val Thr Ile Val Ile Val Gly Met Asn Tyr
245 250 255

Ala Phe Ile Thr Trp Leu Val Lys Ser Arg Leu Lys Arg Leu Cys Ser
260 265 270

Ser Glu Val Gly Leu Leu Lys Asn Ala Glu Arg Glu Gln Glu Ser Glu
275 280 285

Glu Glu Met
290

<210> 30
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 30
Tyr Pro Pro Ser Gly Gly Pro Ala Trp Asp Leu Met Asp His Cys
1 5 10 15

<210> 31
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 31
Cys Leu Lys Asn Ala Glu Arg Glu Gln Glu Ser Glu Glu Glu Met
1 5 10 15

<210> 32
<211> 10320
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (10123)..(10185)
<223> "n" at positions 10123 and 10185 can be any base.

<400> 32
ttcctccgcg aaggctcctt tgatattaat agtgttggtg tcttgaaact gacgtaatgc 60
gcggagactg aggtcctgac aagcgataac atttctgata aagacccgat cttactgcaa 120
tctctagcgt cctcttttt ggtgctgctg gtttctccag acctcgcgtc ctctcgattg 180

ctctctcgcc ttcctatttc ttttttttttt ttttaaacaa aaaacaacac cccctcccct 240
ctcccacccg gcaccgggca catccttgct ctatttcctt tctctttctc tctctctctc 300
tctctctctc ttttttaata agggtggggg agggaaaggg gggggatgca ggaaagacct 360
ttttctctcc cccccgcaat aatccaagat caactctgca aacaacagaa gacggttcat 420
ggctttggcc gccgcgccac catctttcgg gctgccgagg gtgttcttga cgattaatca 480
acagatgtac agatcagctc tcaaaatgtc ttctgtgtct tctgagcgtc ttctaagaca 540
attgcattag cctcctgcta gttgactaat agaattaata attgtaaaaa gcactctaaa 600
gccacatgcc ttatgaagtc aatgctgggt atgattttac aaatatggtc cggaaaaaga 660
acccccctct gagaaacgtt gcaagtgaag gcgagggcca gatcctggag cctataggta 720
cagaaagcaa ggtatctgga aagaacaaag aattttctgc agatcagatg tcagaaaata 780
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<213> Homo sapiens

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Arg Ile Gln Gln Glu Arg Lys Asn Ile Arg Pro Asn Ile Ile Leu Val
35 40 45

Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser Leu Gln Val Met Asn
50 55 60

Lys Thr Arg Lys Ile Met Glu His Gly Gly Ala Thr Phe Ile Asn Ala
65 70 75 80

Phe Val Thr Thr Pro Met Cys Cys Pro Ser Arg Ser Ser Met Leu Thr
85 90 95

Gly Lys Tyr Val His Asn His Asn Val Tyr Thr Asn Asn Glu Asn Cys
100 105 110

Ser Ser Pro Ser Trp Gln Ala Met His Glu Pro Arg Thr Phe Ala Val
115 120 125

Tyr Leu Asn Asn Thr Gly Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu
130 135 140

Asn Glu Tyr Asn Gly Ser Tyr Ile Pro Pro Gly Trp Arg Glu Trp Leu
145 150 155 160

Gly Leu Ile Lys Asn Ser Arg Phe Tyr Asn Tyr Thr Val Cys Arg Asn
165 170 175

Gly Ile Lys Glu Lys His Gly Phe Asp Tyr Ala Lys Asp Tyr Phe Thr
180 185 190

Asp Leu Ile Thr Asn Glu Ser Ile Asn Tyr Phe Lys Met Ser Lys Arg
195 200 205

Met Tyr Pro His Arg Pro Val Met Met Val Ile Ser His Ala Ala Pro
210 215 220

His Gly Pro Glu Asp Ser Ala Pro Gln Phe Ser Lys Leu Tyr Pro Asn
225 230 235 240

Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn Met Asp
245 250 255

Lys His Trp Ile Met Gln Tyr Thr Gly Pro Met Leu Pro Ile His Met
260 265 270

Glu Phe Thr Asn Ile Leu Gln Arg Lys Arg Leu Gln Thr Leu Met Ser
275 280 285

Val Asp Asp Ser Val Glu Arg Leu Tyr Asn Met Leu Val Glu Thr Gly
290 295 300

Glu Leu Glu Asn Thr Tyr Ile Ile Tyr Thr Ala Asp His Gly Tyr His
305 310 315 320

Ile Gly Gln Phe Gly Leu Val Lys Gly Lys Ser Met Pro Tyr Asp Phe
325 330 335

Asp Ile Arg Val Pro Phe Phe Ile Arg Gly Pro Ser Val Glu Pro Gly
340 345 350

Ser Ile Val Pro Gln Ile Val Leu Asn Ile Asp Leu Ala Pro Thr Ile
355 360 365

Leu Asp Ile Ala Gly Leu Asp Thr Pro Pro Asp Val Asp Gly Lys Ser
370 375 380

Val Leu Lys Leu Leu Asp Pro Glu Lys Pro Gly Asn Arg Phe Arg Thr
385 390 395 400

Asn Lys Lys Ala Lys Ile Trp Arg Asp Thr Phe Leu Val Glu Arg Gly
405 410 415

Lys Phe Leu Arg Lys Lys Glu Glu Ser Ser Lys Asn Ile Gln Gln Ser
420 425 430

Asn His Leu Pro Lys Tyr Glu Arg Val Lys Glu Leu Cys Gln Gln Ala
435 440 445

Arg Tyr Gln Thr Ala Cys Glu Gln Pro Gly Gln Lys Trp Gln Cys Ile
450 455 460

Glu Asp Thr Ser Gly Lys Leu Arg Ile His Lys Cys Lys Gly Pro Ser
465 470 475 480

Asp Leu Leu Thr Val Arg Gln Ser Thr Arg Asn Leu Tyr Ala Arg Gly
485 490 495

Phe His Asp Lys Asp Lys Glu Cys Ser Cys Arg Glu Ser Gly Tyr Arg
500 505 510

Ala Ser Arg Ser Gln Arg Lys Ser Gln Arg Gln Phe Leu Arg Asn Gln
515 520 525

Gly Thr Pro Lys Tyr Lys Pro Arg Phe Val His Thr Arg Gln Thr Arg
530 535 540

Ser Leu Ser Val Glu Phe Glu Gly Glu Ile Tyr Asp Ile Asn Leu Glu
545 550 555 560

Glu Glu Glu Glu Leu Gln Val Leu Gln Pro Arg Asn Ile Ala Lys Arg
565 570 575

His Asp Glu Gly His Lys Gly Pro Arg Asp Leu Gln Ala Ser Ser Gly
580 585 590

Gly Asn Arg Gly Arg Met Leu Ala Asp Ser Ser Asn Ala Val Gly Pro
595 600 605

Pro Thr Thr Val Arg Val Thr His Lys Cys Phe Ile Leu Pro Asn Asp
610 615 620

Ser Ile His Cys Glu Arg Glu Leu Tyr Gln Ser Ala Arg Ala Trp Lys
625 630 635 640

Asp His Lys Ala Tyr Ile Asp Lys Glu Ile Glu Ala Leu Gln Asp Lys
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Ile Lys Asn Leu Arg Glu Val Arg Gly His Leu Lys Arg Arg Lys Pro
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Glu Glu Cys Ser Cys Ser Lys Gln Ser Tyr Tyr Asn Lys Glu Lys Gly
675 680 685

Val Lys Lys Gln Glu Lys Leu Lys Ser His Leu His Pro Phe Lys Glu
690 695 700

Ala Ala Gln Glu Val Asp Ser Lys Leu Gln Leu Phe Lys Glu Asn Asn
705 710 715 720

Arg Arg Arg Lys Lys Glu Arg Lys Glu Lys Arg Arg Gln Arg Lys Gly
725 730 735

Glu Glu Cys Ser Leu Pro Gly Leu Thr Cys Phe Thr His Asp Asn Asn
740 745 750

His Trp Gln Thr Ala Pro Phe Trp Asn Leu Gly Ser Phe Cys Ala Cys
755 760 765

Thr Ser Ser Asn Asn Asn Thr Tyr Trp Cys Leu Arg Thr Val Asn Glu
770 775 780

Thr His Asn Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu Tyr
785 790 795 800

Phe Asp Met Asn Thr Asp Pro Tyr Gln Leu Thr Asn Thr Val His Thr
805 810 815

Val Glu Arg Gly Ile Leu Asn Gln Leu His Val Gln Leu Met Glu Leu
820 825 830

Arg Ser Cys Gln Gly Tyr Lys Gln Cys Asn Pro Arg Pro Lys Asn Leu
835 840 845

Asp Val Gly Asn Lys Asp Gly Gly Ser Tyr Asp Leu His Arg Gly Gln
850 855 860

Leu Trp Asp Gly Trp Glu Gly
865 870

<210> 36
<211> 1922
<212> DNA
<213> Homo sapiens

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aa 1922

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<212> DNA
<213> Homo sapiens

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<210> 38
<211> 392
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (111)
<223> "Xaa" at position 111 can be any amino acid.

<400> 38

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Ala Glu Ser Cys Gly Val Gly Gln Gly His Ala Glu Asn Gln Cys Val
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Ser Cys Arg Ala Gly Thr Tyr Tyr Asp Gly Ala Arg Glu Arg Cys Ile
        35                  40                  45

Leu Cys Pro Asn Gly Thr Phe Gln Asn Glu Glu Gly Gln Met Thr Cys
    50                  55                  60

Glu Pro Cys Pro Arg Pro Gly Asn Ser Gly Ala Leu Lys Thr Pro Glu
65                  70                  75                  80

Ala Trp Asn Met Ser Glu Cys Gly Gly Leu Cys Gln Pro Thr Glu Tyr
                85                  90                  95

Ser Ala Asp Gly Phe Ala Pro Cys Gln Leu Cys Ala Leu Gly Xaa Phe
            100                 105                 110

Gln Pro Glu Ala Gly Arg Thr Ser Cys Phe Pro Cys Gly Gly Gly Leu
        115                 120                 125

Ala Thr Lys His Gln Gly Ala Thr Ser Phe Gln Asp Cys Glu Thr Arg
    130                 135                 140

Val Gln Cys Ser Pro Gly His Phe Tyr Asn Thr Thr Thr His Arg Cys
145                 150                 155                 160

Ile Arg Cys Pro Val Gly Thr Tyr Gln Pro Glu Phe Gly Lys Asn Asn
                165                 170                 175

Cys Val Ser Cys Pro Gly Asn Thr Thr Thr Asp Phe Asp Gly Ser Thr
            180                 185                 190

Asn Ile Thr Gln Cys Lys Asn Arg Arg Cys Gly Gly Glu Leu Gly Asp
        195                 200                 205

Phe Thr Gly Tyr Ile Glu Ser Pro Asn Tyr Pro Gly Asn Tyr Pro Ala
    210                 215                 220

Asn Thr Glu Cys Thr Trp Thr Ile Asn Pro Pro Pro Lys Arg Arg Ile
225                 230                 235                 240

Leu Ile Val Val Pro Glu Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly
                245                 250                 255
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Asp Tyr Leu Val Met Arg Lys Thr Ser Ser Ser Asn Ser Val Thr Thr
            260                 265                 270

Tyr Glu Thr Cys Gln Thr Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg
        275                 280                 285

Ser Lys Lys Leu Trp Ile Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala
    290                 295                 300

Arg Gly Phe Gln Val Pro Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu
305                 310                 315                 320

Leu Ile Glu Asp Ile Val Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn
                325                 330                 335

His Gln Glu Ile Leu Lys Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp
            340                 345                 350

Val Leu Ala His Pro Gln Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser
        355                 360                 365

Arg Glu Met Phe Pro Arg Ser Phe Ile Arg Leu Leu Arg Ser Lys Val
    370                 375                 380

Ser Arg Phe Leu Arg Pro Tyr Lys
385                 390


<210> 39
<211> 392
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (111)
<223> "Xaa" at position 111 can be any amino acid.

<400> 39
Met Asn Leu Asp Val Ala Lys Lys Pro Pro Arg Thr Ser Glu Arg Gln
  1               5                  10                  15

Ala Glu Ser Cys Gly Val Gly Gln Gly His Ala Glu Asn Gln Cys Val
             20                  25                  30

Ser Cys Arg Ala Gly Thr Tyr Tyr Asp Gly Ala Arg Glu Arg Cys Ile
         35                  40                  45
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Leu Cys Pro Asn Gly Thr Phe Gln Asn Glu Glu Gly Gln Met Thr Cys
50 55 60

Glu Pro Cys Pro Arg Pro Gly Asn Ser Gly Ala Leu Lys Thr Pro Glu
65 70 75 80

Ala Trp Asn Met Ser Glu Cys Gly Gly Leu Cys Gln Pro Thr Glu Tyr
85 90 95

Ser Ala Asp Gly Phe Ala Pro Cys Gln Leu Cys Ala Leu Gly Xaa Phe
100 105 110

Gln Pro Glu Ala Gly Arg Thr Ser Cys Phe Pro Cys Gly Gly Gly Leu
115 120 125

Ala Thr Lys His Gln Gly Ala Thr Ser Phe Gln Asp Cys Glu Thr Arg
130 135 140

Val Gln Cys Ser Pro Gly His Phe Tyr Asn Thr Thr Thr His Arg Cys
145 150 155 160

Ile Arg Cys Pro Val Gly Thr Tyr Gln Pro Glu Phe Gly Lys Asn Asn
165 170 175

Cys Val Ser Cys Pro Gly Asn Thr Thr Thr Asp Phe Asp Gly Ser Thr
180 185 190

Asn Ile Thr Gln Cys Lys Asn Arg Arg Cys Gly Gly Glu Leu Gly Asp
195 200 205

Phe Thr Gly Tyr Ile Glu Ser Pro Asn Tyr Pro Gly Asn Tyr Pro Ala
210 215 220

Asn Thr Glu Cys Thr Trp Thr Ile Asn Pro Pro Pro Lys Arg Arg Ile
225 230 235 240

Leu Ile Val Val Pro Glu Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly
245 250 255

Asp Tyr Leu Val Met Arg Lys Thr Ser Ser Ser Asn Ser Val Thr Thr
260 265 270

Tyr Glu Thr Cys Gln Thr Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg
275 280 285

Ser Lys Lys Leu Trp Ile Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala
290 295 300

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Arg Gly Phe Gln Val Pro Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu
305                 310                 315                 320

Leu Ile Glu Asp Ile Val Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn
                325                 330                 335

His Gln Glu Ile Leu Lys Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp
            340                 345                 350

Val Leu Ala His Pro Gln Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser
        355                 360                 365

Arg Glu Met Phe Pro Arg Ser Phe Ile Arg Leu Leu Arg Ser Lys Val
    370                 375                 380

Ser Arg Phe Leu Arg Pro Tyr Lys
385                 390
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<210> 40
<211> 162
<212> PRT
<213> Mouse

<400> 40

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Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly Asp Tyr Leu Val Met Arg
             20                  25                  30

Lys Thr Ser Ser Ser Asn Ser Val Thr Thr Tyr Glu Thr Cys Gln Thr
         35                  40                  45

Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg Ser Lys Lys Leu Trp Ile
     50                  55                  60

Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala Arg Gly Phe Gln Val Pro
 65                  70                  75                  80

Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu Leu Ile Glu Asp Ile Val
                85                  90                  95

Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn His Gln Glu Ile Leu Lys
            100                 105                 110

Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp Val Leu Ala His Pro Gln
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115 120 125

Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser Arg Glu Met Phe Pro Arg
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Ser Phe Ile Arg Leu Leu Arg Ser Lys Val Ser Arg Phe Leu Arg Pro
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Tyr Lys

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<212> DNA
<213> Homo sapiens

<400> 41
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<212> DNA
<213> Homo sapiens

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acaaacccga aaagagtgtg a 1041

<210> 43
<211> 346

<212> PRT
<213> Homo sapiens

<400> 43

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Leu Gly Val Arg Gly Ala Pro Cys Glu Ala Val Arg Ile Pro Met Cys
            20                  25                  30

Arg His Met Pro Trp Asn Ile Thr Arg Met Pro Asn His Leu His His
        35                  40                  45

Ser Thr Gln Glu Asn Ala Ile Leu Ala Ile Glu Gln Tyr Glu Glu Leu
    50                  55                  60

Val Asp Val Asn Cys Ser Ala Val Leu Arg Phe Phe Phe Cys Ala Met
65                  70                  75                  80

Tyr Ala Pro Ile Cys Thr Leu Glu Phe Leu His Asp Pro Ile Lys Pro
                85                  90                  95

Cys Lys Ser Val Cys Gln Arg Ala Arg Asp Asp Cys Glu Pro Leu Met
            100                 105                 110

Lys Met Tyr Asn His Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu
        115                 120                 125

Pro Val Tyr Asp Arg Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr
    130                 135                 140

Asp Leu Pro Glu Asp Val Lys Trp Ile Asp Ile Thr Pro Asp Met Met
145                 150                 155                 160

Val Gln Glu Arg Pro Leu Asp Val Asp Cys Lys Arg Leu Ser Pro Asp
                165                 170                 175

Arg Cys Lys Cys Lys Lys Val Lys Pro Thr Leu Ala Thr Tyr Leu Ser
            180                 185                 190

Lys Asn Tyr Ser Tyr Val Ile His Ala Lys Ile Lys Ala Val Gln Arg
        195                 200                 205

Ser Gly Cys Asn Glu Val Thr Thr Val Val Asp Val Lys Glu Ile Phe
    210                 215                 220

Lys Ser Ser Ser Pro Ile Pro Arg Thr Gln Val Pro Leu Ile Thr Asn
225                 230                 235                 240
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Ser Ser Cys Gln Cys Pro His Ile Leu Pro His Gln Asp Val Leu Ile
245 250 255

Met Cys Tyr Glu Trp Arg Ser Arg Met Met Leu Leu Glu Asn Cys Leu
260 265 270

Val Glu Lys Trp Arg Asp Gln Leu Ser Lys Arg Ser Ile Gln Trp Glu
275 280 285

Glu Arg Leu Gln Glu Gln Arg Arg Thr Val Gln Asp Lys Lys Lys Thr
290 295 300

Ala Gly Arg Thr Ser Arg Ser Asn Pro Pro Lys Pro Lys Gly Lys Pro
305 310 315 320

Pro Ala Pro Lys Pro Ala Ser Pro Lys Lys Asn Ile Lys Thr Arg Ser
325 330 335

Ala Gln Lys Arg Thr Asn Pro Lys Arg Val
340 345

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<211> 749
<212> DNA
<213> Homo sapiens

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gaagaaaacc tctggcacat tgacaaatac taaatgtgca agtatataga ttttgtaata 660
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<211> 501
<212> DNA
<213> Homo sapiens

<400> 45
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<210> 46
<211> 166
<212> PRT
<213> Homo sapiens

<400> 46
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Ser Ser Asn Leu Ala Ile Ala Ile Lys Lys Glu Lys Arg Pro Pro Gln
20 25 30

Thr Leu Ser Arg Gly Trp Gly Asp Asp Ile Thr Trp Val Gln Thr Tyr
35 40 45

Glu Glu Gly Leu Phe Tyr Ala Gln Lys Ser Lys Lys Pro Leu Met Val
50 55 60

Ile His His Leu Glu Asp Cys Gln Tyr Ser Gln Ala Leu Lys Lys Val
65 70 75 80

Phe Ala Gln Asn Glu Glu Ile Gln Glu Met Ala Gln Asn Lys Phe Ile
85 90 95

Met Leu Asn Leu Met His Glu Thr Thr Asp Lys Asn Leu Ser Pro Asp
100 105 110

Gly Gln Tyr Val Pro Arg Ile Met Phe Val Asp Pro Ser Leu Thr Val
115 120 125

Arg Ala Asp Ile Ala Gly Arg Tyr Ser Asn Arg Leu Tyr Thr Tyr Glu
130 135 140

Pro Arg Asp Leu Pro Leu Leu Ile Glu Asn Met Lys Lys Ala Leu Arg
145 150 155 160

Leu Ile Gln Ser Glu Leu
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<210> 47
<211> 3493
<212> DNA
<213> Homo sapiens

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<210> 48
<211> 925
<212> PRT
<213> Homo sapiens

<400> 48
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Arg Ser His Ala Ala Glu Ala Pro Gly Asp Pro Gln Ala Ala Ala Ser
35 40 45

Leu Leu Ala Pro Met Asp Val Gly Glu Glu Pro Leu Glu Lys Ala Ala
50 55 60

Arg Ala Arg Thr Ala Lys Asp Pro Asn Thr Tyr Lys Val Leu Ser Leu
65 70 75 80

Val Leu Ser Val Cys Val Leu Thr Thr Ile Leu Gly Cys Ile Phe Gly
85 90 95

Leu Lys Pro Ser Cys Ala Lys Glu Val Lys Ser Cys Lys Gly Arg Cys
100 105 110

Phe Glu Arg Thr Phe Gly Asn Cys Arg Cys Asp Ala Ala Cys Val Glu
115 120 125

Leu Gly Asn Cys Cys Leu Asp Tyr Gln Glu Thr Cys Ile Glu Pro Glu
130 135 140

His Ile Trp Thr Cys Asn Lys Phe Arg Cys Gly Glu Lys Arg Leu Thr
145 150 155 160

Arg Ser Leu Cys Ala Cys Ser Asp Asp Cys Lys Asp Lys Gly Asp Cys
165 170 175

Cys Ile Asn Tyr Ser Ser Val Cys Gln Gly Glu Lys Ser Trp Val Glu
180 185 190

Glu Pro Cys Glu Ser Ile Asn Glu Pro Gln Cys Pro Ala Gly Phe Glu
195 200 205

Thr Pro Pro Thr Leu Leu Phe Ser Leu Asp Gly Phe Arg Ala Glu Tyr
210 215 220

Leu His Thr Trp Gly Gly Leu Leu Pro Val Ile Ser Lys Leu Lys Lys
225 230 235 240

Cys Gly Thr Tyr Thr Lys Asn Met Arg Pro Val Tyr Pro Thr Lys Thr
245 250 255

Phe Pro Asn His Tyr Ser Ile Val Thr Gly Leu Tyr Pro Glu Ser His
260 265 270

Gly Ile Ile Asp Asn Lys Met Tyr Asp Pro Lys Met Asn Ala Ser Phe
275 280 285

Ser Leu Lys Ser Lys Glu Lys Phe Asn Pro Glu Trp Tyr Lys Gly Glu
290 295 300

Pro Ile Trp Val Thr Ala Lys Tyr Gln Gly Leu Lys Ser Gly Thr Phe
305 310 315 320

Phe Trp Pro Gly Ser Asp Val Glu Ile Asn Gly Ile Phe Pro Asp Ile
325 330 335

Tyr Lys Met Tyr Asn Gly Ser Val Pro Phe Glu Glu Arg Ile Leu Ala
340 345 350

Val Leu Gln Trp Leu Gln Leu Pro Lys Asp Glu Arg Pro His Phe Tyr
355 360 365

Thr Leu Tyr Leu Glu Glu Pro Asp Ser Ser Gly His Ser Tyr Gly Pro
370 375 380

Val Ser Ser Glu Val Ile Lys Ala Leu Gln Arg Val Asp Gly Met Val
385 390 395 400

Gly Met Leu Met Asp Gly Leu Lys Glu Leu Asn Leu His Arg Cys Leu
405 410 415

Asn Leu Ile Leu Ile Ser Asp His Gly Met Glu Gln Gly Ser Cys Lys
420 425 430

Lys Tyr Ile Tyr Leu Asn Lys Tyr Leu Gly Asp Val Lys Asn Ile Lys
435 440 445

Val Ile Tyr Gly Pro Ala Ala Arg Leu Arg Pro Ser Asp Val Pro Asp
450 455 460

Lys Tyr Tyr Ser Phe Asn Tyr Glu Gly Ile Ala Arg Asn Leu Ser Cys
465 470 475 480

Arg Glu Pro Asn Gln His Phe Lys Pro Tyr Leu Lys His Phe Leu Pro
485 490 495

Lys Arg Leu His Phe Ala Lys Ser Asp Arg Ile Glu Pro Leu Thr Phe
500 505 510

Tyr Leu Asp Pro Gln Trp Gln Leu Ala Leu Asn Pro Ser Glu Arg Lys
515 520 525

Tyr Cys Gly Ser Gly Phe His Gly Ser Asp Asn Val Phe Ser Asn Met
530 535 540

Gln Ala Leu Phe Val Gly Tyr Gly Pro Gly Phe Lys His Gly Ile Glu
545 550 555 560

Ala Asp Thr Phe Glu Asn Ile Glu Val Tyr Asn Leu Met Cys Asp Leu
565 570 575

Leu Asn Leu Thr Pro Ala Pro Asn Asn Gly Thr His Gly Ser Leu Asn
580 585 590

His Leu Leu Lys Asn Pro Val Tyr Thr Pro Lys His Pro Lys Glu Val
595 600 605

His Pro Leu Val Gln Cys Pro Phe Thr Arg Asn Pro Arg Asp Asn Leu
610 615 620

Gly Cys Ser Cys Asn Pro Ser Ile Leu Pro Ile Glu Asp Phe Gln Thr
625 630 635 640

Gln Phe Asn Leu Thr Val Ala Glu Glu Lys Ile Ile Lys His Glu Thr
645 650 655

Leu Pro Tyr Gly Arg Pro Arg Val Leu Gln Lys Glu Asn Thr Ile Cys
660 665 670

Leu Leu Ser Gln His Gln Phe Met Ser Gly Tyr Ser Gln Asp Ile Leu
675 680 685

Met Pro Leu Trp Thr Ser Tyr Thr Val Asp Arg Asn Asp Ser Phe Ser
690 695 700

Thr Glu Asp Phe Ser Asn Cys Leu Tyr Gln Asp Phe Arg Ile Pro Leu
705 710 715 720

Ser Pro Val His Lys Cys Ser Phe Tyr Lys Asn Asn Thr Lys Val Ser
725 730 735

Tyr Gly Phe Leu Ser Pro Pro Gln Leu Asn Lys Asn Ser Ser Gly Ile
740 745 750

Tyr Ser Glu Ala Leu Leu Thr Thr Asn Ile Val Pro Met Tyr Gln Ser
755 760 765

Phe Gln Val Ile Trp Arg Tyr Phe His Asp Thr Leu Leu Arg Lys Tyr
770 775 780

Ala Glu Glu Arg Asn Gly Val Asn Val Val Ser Gly Pro Val Phe Asp
785 790 795 800

Phe Asp Tyr Asp Gly Arg Cys Asp Ser Leu Glu Asn Leu Arg Gln Lys
805 810 815

Arg Arg Val Ile Arg Asn Gln Glu Ile Leu Ile Pro Thr His Phe Phe
820 825 830

Ile Val Leu Thr Ser Cys Lys Asp Thr Ser Gln Thr Pro Leu His Cys
835 840 845

Glu Asn Leu Asp Thr Leu Ala Phe Ile Leu Pro His Arg Thr Asp Asn
850 855 860

Ser Glu Ser Cys Val His Gly Lys His Asp Ser Ser Trp Val Glu Glu
865 870 875 880

Leu Leu Met Leu His Arg Ala Arg Ile Thr Asp Val Glu His Ile Thr
885 890 895

Gly Leu Ser Phe Tyr Gln Gln Arg Lys Glu Pro Val Ser Asp Ile Leu
900 905 910

Lys Leu Lys Thr His Leu Pro Thr Phe Ser Gln Glu Asp
915 920 925

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<211> 2709
<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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35 40 45

Gly Pro Lys Tyr Met Arg Asn Lys Gln Pro Phe Ser Cys Arg Gly Ile
50 55 60

Leu Val Val Tyr Asn Leu Gly Leu Thr Leu Leu Ser Leu Tyr Met Phe
65 70 75 80

Cys Glu Leu Val Thr Gly Val Trp Glu Gly Lys Tyr Asn Phe Phe Cys
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Gln Gly Thr Arg Thr Ala Gly Glu Ser Asp Met Lys Ile Ile Arg Val
100 105 110

Leu Trp Trp Tyr Tyr Phe Ser Lys Leu Ile Glu Phe Met Asp Thr Phe
115 120 125

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Tyr His His Ala Ser Met Leu Asn Ile Trp Trp Phe Val Met Asn Trp
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Val Pro Cys Gly His Ser Tyr Phe Gly Ala Thr Leu Asn Ser Phe Ile
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His Val Leu Met Tyr Ser Tyr Tyr Gly Leu Ser Ser Val Pro Ser Met
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Arg Pro Tyr Leu Trp Trp Lys Lys Tyr Ile Thr Gln Gly Gln Leu Leu
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Gln Phe Val Leu Thr Ile Ile Gln Thr Ser Cys Gly Val Ile Trp Pro
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Cys Thr Phe Pro Leu Gly Trp Leu Tyr Phe Gln Ile Gly Tyr Met Ile
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Ser Leu Ile Ala Leu Phe Thr Asn Phe Tyr Ile Gln Thr Tyr Asn Lys
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Lys Gly Ala Ser Arg Arg Lys Asp His Leu Lys Asp His Gln Asn Gly
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Ser Met Ala Ala Val Asn Gly His Thr Asn Ser Phe Ser Pro Leu Glu
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<212> DNA
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<212> DNA
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<210> 53
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (3)
<223> "Xaa" at position 3 can be any amino acid

<220>
<223> Description of Artificial Sequence: Ctyokine receptor exctracellular motif found in many species.

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